

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 16:32:24 ; Search time 68 Seconds  
(Without alignments)  
2047.955 Million cell updates/sec

Title: us-09-635-501-2

Perfect score: 4291

Sequence: 1 MSSSSWLLSLVAVTAQAQST.....ISKGENNPGFQNTDDVQTSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	4291	100.0	805	4	Q9NRA7	Q9nra7 homo sapien
2	4288	99.9	805	4	Q9BYF1	Q9byf1 homo sapien
3	4281	99.8	804	4	Q9UFZ6	Q9ufz6 homo sapien
4	3485	81.2	798	11	Q99N71	Q99n71 mus musculus
5	1539	35.9	353	11	Q99N70	Q99n70 mus musculus
6	1336	31.1	732	6	Q9GLN6	Q9gln6 pan troglod
7	1329	31.0	1304	6	Q9GLN7	Q9gln7 pan troglod
8	1310	30.5	1313	11	Q9EQM9	Q9eqm9 rattus norv
9	1303	30.4	694	4	Q15540	Q15540 homo sapien
10	1089.5	25.4	648	5	Q9NDS8	Q9nds8 bombyx mori
11	1086	25.3	615	5	Q9NKR4	Q9nkr4 drosophila
12	1057	24.6	660	5	Q17248	Q17248 boophilus m
13	1030	24.0	630	5	Q24222	Q24222 drosophila
14	1028	24.0	630	5	Q9VLJ6	Q9vlj6 drosophila
15	1004	23.4	249	11	Q9DL76	Q9dl76 mus musculus
16	841	19.6	792	5	Q9VJV1	Q9vjv1 drosophila

17 642.5 15.0 907 5 Q18581  
18 502.5 11.7 661 5 Q9V520  
19 476 11.1 611 5 Q9VJV2  
20 434.5 10.1 202 11 Q64603  
21 409.5 9.5 628 5 Q9W021  
22 408.5 9.5 628 5 Q9S059  
23 390 9.1 222 11 Q9ESG3  
24 387 9.0 222 4 Q9HJH8  
25 386 9.0 222 11 Q9ESG4  
26 306.5 7.1 121 6 Q9BDG1  
27 280.5 6.5 135 4 Q16425  
28 251.5 5.9 157 11 Q61265  
29 239 5.6 75 5 Q9TX66  
30 157 3.7 532 16 Q9KRV0  
31 152.5 3.6 734 5 Q9NKE3  
32 147 3.4 54 6 Q95161  
33 147 3.4 502 16 Q92AC3  
34 139 3.2 608 16 Q9PR80  
35 136 3.2 611 16 Q9PPW8  
36 130.5 3.0 461 2 Q9KI52  
37 127.5 3.0 3574 10 Q9AUB4  
38 127 3.0 779 5 Q9XY88  
39 124.5 2.9 987 11 Q61636  
40 124.5 2.9 3429 11 Q08614  
41 124 2.9 53 6 Q18865  
42 124 2.9 538 17 Q9VB20  
43 123.5 2.9 902 17 Q97YV0  
44 123.5 2.9 3419 11 Q55147  
45 123.5 2.9 5303 5 Q9V628

## ALIGNMENTS

## RESULT 1

Q9NRA7 ID Q9NRA7 PRELIMINARY; PRT; 805 AA.  
AC Q9NRA7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ANGIOTENSIN CONVERTING ENZYME-LIKE PROTEIN (ACE-RELATED  
DE CARBOXYPEPTIDASE ACE2).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-LYMPHOMA;  
RA Tippi S.R., Hooper N.M., Hyde R.J., Christie G., Karran E.,  
RA Turner A.J.;  
RT "A Human Homolog of Angiotensin Converting Enzyme - Cloning and  
RT Functional Expression As A Captopril-Insensitive Carboxypeptidase.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RN  
RP SEQUENCE FROM N.A.  
RA Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,  
RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,  
RA Breitbart R.E., Acton S.;  
RT "A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to  
RT angiotensin-9.";  
RL Circ. Res. 0:0-0(2000).  
DR EMBL; AF241254; AAF78220.1; -;  
DR EMBL; AF291820; AAF99721.1; -;  
DR MEROPS; M02.006; -;  
DR InterPro; IPR001548; Peptidase\_M2.  
DR InterPro; IPR000130; Zn\_Mtpeptdse.  
DR Pfam; PF01401; Peptidase\_M2; 1.  
DR PRINTS; PR00791; PEPTIDASEA.  
DR ProDom; PD004184; Peptidase\_M2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Carboxypeptidase.



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QY 721 SLEFLGIQTLGPPNPPVSIWLVFVGMVGVVGVIVILFTGIRDRKKKARSGENP 780
Db 721 SLEFLGIQTLGPPNPPVSIWLVFVGMVGVVGVIVILFTGIRDRKKKARSGENP 780
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
Db 781 YASIDISKGENNPGFQNTDDVQTSF 805
RESULT 3
Q9UF26
ID Q9UF26 PRELIMINARY; PRT; 804 AA.
AC Q9UF26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 92.3 KDA PROTEIN (FRAGMENT).
GN DKEP434A014.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL110224; CAB53682.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; Peptidase_M2.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;
Query Match 99.98; Score 4281; DB 4; Length 804;
Best Local Similarity 99.98; Pred. No. 1.1e-304;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 SSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHAEADLFYQSSLASWNYNTITEENVQ 61
Db 1 SSSSWLLLSLVAVTAAHSTIEEQAKTFLDKFNHAEADLFYQSSLASWNYNTITEENVQ 60
QY 62 MNNAGDKWSAFLKEQSTLAQMPLOEIQLNLTVKLQALQNGSSVLSDEKSKRLNTILN 121
Db 61 MNNAGDKWSAFLKEQSTLAQMPLOEIQLNLTVKLQALQNGSSVLSDEKSKRLNTILN 120
QY 122 TMSITSTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWSRSEVQKQLRPLYE 181
Db 121 TMSITSTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWSRSEVQKQLRPLYE 180
QY 182 EYVLKNEMARAHYEDYGDYWRGDYEVNGVDYDYSRGQIEDVEHFEETKPLYEHLH 241
Db 181 EYVLKNEMARAHYEDYGDYWRGDYEVNGVDYDYSRGQIEDVEHFEETKPLYEHLH 240
QY 242 AYVRKLMNAPYSYISPGCLPAHLGLDMGGRFWTNLSLVTPFGQKPNIDVTDAMVQQA 301
Db 241 AYVRKLMNAPYSYISPGCLPAHLGLDMGGRFWTNLSLVTPFGQKPNIDVTDAMVQQA 300
QY 302 WDAQRIFKBAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLGKDFRILMC 361
Db 301 WDAQRIFKBAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLGKDFRILMC 360
QY 362 TKVTMDDFLTAHEMGHIQYDMAYAAQFFLLRNGANEGFHEAVGIMSLSAATPKHLKSI 421
Db 361 TKVTMDDFLTAHEMGHIQYDMAYAAQFFLLRNGANEGFHEAVGIMSLSAATPKHLKSI 420
QY 422 GLSPDQEDNETEINFLKQALTIQVGLPFTYMLEKRWVFKGEIPKQDQWKKWEMK 481
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Db 421 GLSPDQEDNETEINFLKQALTIQVGLPFTYMLEKRWVFKGEIPKQDQWKKWEMK 480
QY 482 REIVGVVEVPVPHDQCDPASLRFHVSNDYSFIRYTRTLYQFOFQALCOAAKHGEP LHK 541
Db 481 REIVGVVEVPVPHDQCDPASLRFHVSNDYSFIRYTRTLYQFOFQALCOAAKHGEP LHK 540
QY 542 CDSINSTEAGOKLFLNMLRLGKSEPTLALENVVGAKNMVRPPLLNFPELFTWLKDQKN 601
Db 541 CDSINSTEAGOKLFLNMLRLGKSEPTLALENVVGAKNMVRPPLLNFPELFTWLKDQKN 600
QY 602 SFVGSTDSWPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMROYFLKVKNO 661
Db 601 SFVGSTDSWPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMROYFLKVKNO 660
QY 662 MILFGEEDVRANLKPRISFNFFVAPKNVSDIIPREVEKAIKMSRINDAFRLDMS 721
Db 661 MILFGEEDVRANLKPRISFNFFVAPKNVSDIIPREVEKAIKMSRINDAFRLDMS 720
QY 722 LEFLGIQTLGPPNPPVSIWLVFVGMVGVVGVIVILFTGIRDRKKKARSGENP 781
Db 721 LEFLGIQTLGPPNPPVSIWLVFVGMVGVVGVIVILFTGIRDRKKKARSGENP 780
QY 782 ASIDISKGENNPGFQNTDDVQTSF 805
Db 781 ASIDISKGENNPGFQNTDDVQTSF 804
RESULT 4
Q99N71
ID Q99N71 PRELIMINARY; PRT; 798 AA.
AC Q99N71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANIGOTENSIN-CONVERTING ENZYME-RELATED CARBOXYPEPTIDASE.
GN ACB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053181; BAB40431.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; Peptidase_M2.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 798 AA; 91943 MW; 403AEA29D55725A4 CRC64;
Query Match 81.2%; Score 3485; DB 11; Length 798;
Best Local Similarity 82.2%; Pred. No. 1.9e-246;
Matches 644; Conservative 58; Mismatches 81; Indels 0; Gaps 0;
QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHAEADLFYQSSLASWNYNTITEENVQ 60
Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHAEADLFYQSSLASWNYNTITEENVQ 60
QY 61 MNNAGDKWSAFLKEQSTLAQMPLOEIQLNLTVKLQALQNGSSVLSDEKSKRLNTIL 120
Db 61 MNNAGDKWSAFLKEQSTLAQMPLOEIQLNLTVKLQALQNGSSVLSDEKSKRLNTIL 120
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QY 121 NTMSTIYTGKVCNPNPQECLELPEGLNEIMANSLDYNRLWAWESWSEVKGQRLPLY 180
Db 121 NTMSTIYTGKVCNPNPQECLELPEGLDEIMATSTYDYNRLWAWESWSEVKGQRLPLY 180
QY 181 EYVVLKNEMARANHYEDYDGYWRGDDYVNGVDGYDYSRGQLIEDVEHTFBEIKPLYEHL 240
Db 181 EYVVLKNEMARANHYEDYDGYWRGDDYVNGVDGYDYSRGQLIEDVEHTFBEIKPLYEHL 240
QY 241 HAYVRKLMNAPSYISPIGCLPAHLGLDMGRFTNLYSLVPPGQKPNIDVTDAMVDQ 300
Db 241 HAYVRKLMNAPSYISPIGCLPAHLGLDMGRFTNLYSLVPPGQKPNIDVTDAMVDQ 300
QY 301 AWAQRIFFKAEEFFVSVGLPNTQGFWNSMLTDPGNVOKAVCHPTAMDGLKGDFRILM 360
Db 301 AWAQRIFFKAEEFFVSVGLPNTQGFWNSMLTDPGNVOKAVCHPTAMDGLKGDFRILM 360
QY 361 CTKYTMDDFLTAHHEMGIQYDMAYAAQFFLLRNGANECHFPAVGGEIMSLSAATPKHLKS 420
Db 361 CTKYTMDDFLTAHHEMGIQYDMAYAAQFFLLRNGANECHFPAVGGEIMSLSAATPKHLKS 420
QY 421 IGLLSPQFQEDNETEINFLKQALTYVGTLPPTYMLEKRWVVFGEIPKQDQMKKWWEM 480
Db 421 IGLLSPQFQEDNETEINFLKQALTYVGTLPPTYMLEKRWVVFGEIPKQDQMKKWWEM 480
QY 481 KREIVGVVPEPHDETCDPASLFHVSNDYSFIRYTRTYLQFQFQALCQAAKHGCPH 540
Db 481 KREIVGVVPEPHDETCDPASLFHVSNDYSFIRYTRTYLQFQFQALCQAAKHGCPH 540
QY 541 KDISNSTEAGOKFLNMLKSGSEPTLALENVGAKNNVRPLNAYFELFWLKDQNK 600
Db 541 KDISNSTEAGOKFLNMLKSGSEPTLALENVGAKNNVRPLNAYFELFWLKDQNK 600
QY 601 NSFYGWSTNSPYADQSIKVRISLKSALGDKAYEWNDNMYLFRSSVAYAMROYFLKVKN 660
Db 601 NSFYGWSTNSPYADQSIKVRISLKSALGANAYEWNNEMELFRSSVAYAMRKVFSIKN 660
QY 661 QMILFGEDVRVANKPRISNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDN 720
Db 661 QMILFGEDVRVANKPRISNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDN 720
QY 721 SLEFLGTOPTLGPNNQPVSTWLVFGVVGVIWGVILVFTGIRDKKKKARSGENP 780
Db 721 SLEFLGTOPTLGPNNQPVSTWLVFGVVGVIWGVILVFTGIRDKKKKARSGENP 780
QY 781 YAS 783
Db 781 YDS 783
RESULT 5
Q99N70 PRELIMINARY; PRT; 353 AA.
AC Q99N70;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANIGOTENSIN-CONVERTING ENZYME-RELATED CARBOXYPEPTIDASE.
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Yamada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Suzuki Y., Hanaoka K., Yamada Y.;
RT "Molecular cloning of ACE2.";
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RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053182; BAB40432.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPITASEA.
DR PRODOM; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 353 AA; 40442 MW; DL7B71141EE4AF5B CRC64;

Query Match 35.9%; Score 1539; DB 11; Length 353;
Best Local Similarity 81.2%; Pred. No. 1.5e-104;
Matches 285; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFDLKFNHEADLFFYOSSLASWNYNTNITEENVQ 60
Db 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFDLKFNHEADLFFYOSSLASWNYNTNITEENVQ 60
QY 61 MNMAGDKWSAFLEKQSTLAQMYPLQEIQLTYKLOLQALQOQSSVLSDEKSKRLNTIL 120
Db 61 KMSEAAAKWSAFYEEQSKTAQSPSLOEIQTPIIKRQLQALQOQSSVLSADKKNKQNTIL 120
QY 121 NTMSTIYTGKVCNPNPQECLELPEGLNEIMANSLDYNRLWAWESWSEVKGQRLPLY 180
Db 121 NTMSTIYTGKVCNPNPQECLELPEGLDEIMATSTYDYNRLWAWESWSEVKGQRLPLY 180
QY 181 EYVVLKNEMARANHYEDYDGYWRGDDYVNGVDGYDYSRGQLIEDVEHTFBEIKPLYEHL 240
Db 181 EYVVLKNEMARANHYEDYDGYWRGDDYVNGVDGYDYSRGQLIEDVEHTFBEIKPLYEHL 240
QY 241 HAYVRKLMNAPSYISPIGCLPAHLGLDMGRFTNLYSLVPPGQKPNIDVTDAMVDQ 300
Db 241 HAYVRKLMNAPSYISPIGCLPAHLGLDMGRFTNLYSLVPPGQKPNIDVTDAMVDQ 300
QY 301 AWAQRIFFKAEEFFVSVGLPNTQGFWNSMLTDPGNVOKAVCHPTAMD 351
Db 301 AWAQRIFFKAEEFFVSVGLPNTQGFWNSMLTDPGNVOKAVCHPTAMD 351

RESULT 6
Q9GLN6 PRELIMINARY; PRT; 732 AA.
AC Q9GLN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DIPEPTIDYL CARBOXY PEPTIDASE 1 TESTICULAR FORM.
GN DCPL.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunevaltre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin-angiotensin system."
RL Genomics 69:14-26(2000).
DR EMBL; AF193473; AAG31359.1; JOINED.
DR EMBL; AF193474; AAG31359.1; JOINED.
DR EMBL; AF193475; AAG31359.1; JOINED.
DR EMBL; AF193476; AAG31359.1; JOINED.
DR EMBL; AF193477; AAG31359.1; JOINED.
DR EMBL; AF193478; AAG31359.1; JOINED.
DR EMBL; AF193479; AAG31359.1; JOINED.
DR EMBL; AF193480; AAG31359.1; JOINED.
DR EMBL; AF193481; AAG31359.1; JOINED.
DR EMBL; AF193482; AAG31359.1; JOINED.
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DR EMBL; AF193483; AAG31359.1; JOINED.
DR EMBL; AF193484; AAG31359.1; JOINED.
DR EMBL; AF193485; AAG31359.1; JOINED.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 732 AA; 83428 MW; C43D06443A47E74B CRC64;

Query Match 31.1%; Score 1336; DB 6; Length 732;
Best Local Similarity 41.6%; Pred. No. 3.2e-89;
Matches 258; Conservative 119; Mismatches 205; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKFLDKENHEADLFYQSSLASWNYNTNITEE-----NVQNM 62
Db 61 TSAQSPNLVTDKAEAKFVEYDRTSQVWNEYAEANNYNITTTETSKILLQKNQIA 120
QY 63 NNAGDKWSAFLEKQSTLAQNTPLQEQNLTKVQLQALQOQSSVLSDEKSKRLNTILNT 122
Db 121 NHT-----LKYGTQARRDVLQNTTIKRIKKVQDLRAALPAQELEEVNKLDD 172
QY 123 MSTIYSTGKVCNPNPQECILLECLNEIMANSLDYNERLWAWESRSEVGKQLRPLYEE 182
Db 173 METTYSVATVCHTNG--SCLOEPDLTNVMTSRKYEDLLWAWEGWRDKAGRAILOFYPK 230
QY 183 YVVLKNDMARANHYEDYGYWRGDEYVNGVDGYDYSRGOLIEDVHTFEIKPLYEHLHA 242
Db 231 YVELINQARLNGYVDAGDSWRSMEYPSLE-----QDLERLFOELQPLYLNLHA 280
QY 243 YVRACLNNAY-PSYISPIGCLPAHLGDMGFRFTNLYSLVFPQGNIDVTDMVDDQA 301
Db 281 YVRALHRYHGAQHINLEGPIPAHLGDMGFRFTNLYSLVFPQGNIDVTDMVDDQA 340
QY 302 WDAQRLFKAEKFSVYGLPNMTGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DPRILM 360
Db 341 WTPRRFKFADDEFTSLGLLPVFPFVFNKSMLEKPTDGRVYVCHASAWDFYNGKDFRIK 400
QY 361 CTKVTMDDFLTAHEMCHIOVDMAAQAPELLRNCANGFHEAVGEIMSLSATPKHLKS 420
Db 401 CTTVNLEDLVVAHEMCHIQFYMOYKDLPLVALREGANPGFHEAIGDVLALSYSTPKHLHS 460
QY 421 IGLLSPDFQEDNETEINFLKQALITVGLTPTVYMLEKRWNVFKEIPKQDMMKKWEM 480
Db 461 LNLSEGGSD-EHDIINFLKMDKIAFIPFSYLVQDQRRVFDGSIKENYQWNSL 519
QY 481 KRIVGVVEVPDHEITCDPASLPHSVNDYSFIRYTRTLQFOFQALCOAAKHGRLH 540
Db 520 RLKYQGLCPVPRTQGFDPFCAKPHIPSSVPYIRYFVSFILOFQFHEALCQAAGHTGPLH 579
QY 541 KCDISNSTEAGOKLFNMLRLGKSEPTWLTALENVVGAKNVVRPLNLYTEPLFTWLKDQNK 600
Db 580 KCDIYOSKEAGQALATAMKLGFSRNPPEAMOLITGQPNMSASAMLSYKPLDLDLRTENE 639
QY 601 --NSFVGW-STDWSPYADQS 617
Db 640 LHCEKLGWQVNYNTPNSARS 659

RESULT 7
Q9GLN7 PRELIMINARY; PRT; 1304 AA.
AC Q9GLN7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DIPEPTIDYL CARBOXY PEPTIDASE 1.
GN DCPI.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
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[1] SEQUENCE FROM N.A.
RP MEDLINE=20469400; PubMed=11013071;
RX Dufour C., Casane D., Wickings J., Corvol P.,
RA Jeunemaitre X.,
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin angiotensin system.";
RL Genomics 69:14-26(2000).
DR EMBL; AF193486; AAG31358.1; JOINED.
DR EMBL; AF193462; AAG31358.1; JOINED.
DR EMBL; AF193463; AAG31358.1; JOINED.
DR EMBL; AF193464; AAG31358.1; JOINED.
DR EMBL; AF193465; AAG31358.1; JOINED.
DR EMBL; AF193466; AAG31358.1; JOINED.
DR EMBL; AF193467; AAG31358.1; JOINED.
DR EMBL; AF193468; AAG31358.1; JOINED.
DR EMBL; AF193469; AAG31358.1; JOINED.
DR EMBL; AF193470; AAG31358.1; JOINED.
DR EMBL; AF193471; AAG31358.1; JOINED.
DR EMBL; AF193472; AAG31358.1; JOINED.
DR EMBL; AF193473; AAG31358.1; JOINED.
DR EMBL; AF193474; AAG31358.1; JOINED.
DR EMBL; AF193475; AAG31358.1; JOINED.
DR EMBL; AF193476; AAG31358.1; JOINED.
DR EMBL; AF193477; AAG31358.1; JOINED.
DR EMBL; AF193478; AAG31358.1; JOINED.
DR EMBL; AF193479; AAG31358.1; JOINED.
DR EMBL; AF193481; AAG31358.1; JOINED.
DR EMBL; AF193482; AAG31358.1; JOINED.
DR EMBL; AF193483; AAG31358.1; JOINED.
DR EMBL; AF193484; AAG31358.1; JOINED.
DR EMBL; AF193485; AAG31358.1; JOINED.
DR MEROPS; M02.001; -.
DR MEROPS; M02.004; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01401; Peptidase_M2; 2.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 1304 AA; 149369 MW; DCF728D0BA0F1314 CRC64;

Query Match 31.0%; Score 1329; DB 6; Length 1304;
Best Local Similarity 41.6%; Pred. No. 2.4e-88;
Matches 254; Conservative 118; Mismatches 205; Indels 34; Gaps 9;

QY 20 TIEQAKFLDKENHEADLFYQSSLASWNYNTNITEE-----NVQNMNAGDKWSA 71
Db 642 TDEAKSFVEYDRTSQVWNEYAEANNYNITTTETSKILLQKNQIAHNT----- 695
QY 72 FLKEQSTLAQNTPLQEQNLTKVQLQALQOQSSVLSDEKSKRLNTILNTMSTIYSTGK 131
Db 696 --LKYGTQARRDVLQNTTIKRIKKVQDLRAALPAQELEEVNKLDDMETTYSVAT 753
QY 132 VCNPNPQECILLECLNEIMANSLDYNERLWAWESRSEVGKQLRPLYEYVVLKNEA 191
Db 754 VCHTNG--SCLOEPDLTNVMTSRKYEDLLWAWEGWRDKAGRAILOFYPRVELINQAA 811
QY 192 RANHYEDYGYWRGDEYVNGVDGYDYSRGOLIEDVHTFEIKPLYEHLHAYVRAKLMA 251
Db 812 RLNGYVDAGDSWRSMEYTPSLE-----QDLERLFOELQPLYLNLHAYVRRALHRH 861
QY 252 Y-PSYISPIGCLPAHLGDMGFRFTNLYSLVFPQGNIDVTDMVDDQAQRIKFE 310
Db 862 YGAQHINLEGPIPAHLGDMGFRFTNLYSLVFPQGNIDVTDMVDDQAQRIKFE 921
QY 311 AEKFFVSVGLPNMTGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DPRILMCTKVTMDDF 369
Db 922 ADFFTSGLLPVPPPEFVFNKSMLEKPTDGRVYVCHASAWDFYNGKDFRIKQCTVTNLEDL 981
QY 370 LTAHEMCHIQVDMAAQAQPLLRNCANGFHEAVGEIMSLSATPKHLKSIGLLSPDFQ 429
Db 429 LTAHEMCHIQVDMAAQAQPLLRNCANGFHEAVGEIMSLSATPKHLKSIGLLSPDFQ 429
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QY 276 TNLVSLVTPFGKPNIDVTAMVQDAQDAORIFKAEKFFVSVGLPMTQGFWNSMLTD 335
Db 277 SNYIDLVPFSPASMDTTEAMLKCGTWRMFKKADDEFTSLGLLPVPPFERNKSMLEK 336
QY 336 PGNVQKAVCHPTADWLGGK--DFRILMCTKV7MDDFLTAHHEMGIQYDMAYAAQPFLLRN 394
Db 337 PTGREVYVCHASAMDFYNGKDFRIKQCTVYNLEDLVAAHHEMGIQYFQYKDKLPVALRE 396
QY 395 GANEGFHEAVEGMSLSAATPKHLKSIIGLLSPDFQEDNTEINFLKQALTVIGTLPFTY 454
Db 397 GANPGFHEAGDVLYALSVSTPKHLHSLNLSSEGGSD--EHDINFLMKMLDKTAFIPFSY 455
QY 455 MLEKRWVWFKGEIPKQDMKKWEMKREIVGVVPPVPHIDETCYCDPASLFHVSNDYSFIR 514
Db 456 LVQWRVRVFDGSTKENYNEWSLRUKYOGCLCPPVPRTOGDFDPAKPHIPSSVPYIR 515
QY 515 YYTRTYLQFOEQEALCAAKEGHLKCDISNSTEAGOKLFNMLRLGKSEPTWFLALENVV 574
Db 516 YFVSFLIQFQFHEALCAAAGHTGPHLKCDIYQSKAGORLATAMKLGFRPWPPEAMQLIT 575
QY 575 GAKNMVRLNLTPELFTWLDQNK--NSFVGW--STWSPYADQS 617
Db 576 GQPNMSASAMLSYFKPLLDLWRLTENELHGEKLGWQYNWTPNSARS 621

RESULT 10
Q9NDS8 ID Q9NDS8 PRELIMINARY; PRT; 648 AA.
AC Q9NDS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ECDYSTEROID-INDUCIBLE ANGIOTENSIN-CONVERTING ENZYME-RELATED GENE
DS PRODUCT.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C108; TISSUE=WING IMAGINAL DISK;
RX MEDLINE=20556050; PubMed=11102839;
RA Quan G.X., Mita K., Okano K., Shimada T., Ugajin N., Xia Z., Goto N.,
RA Kanke E., Kawasaki H.;
RT *Isolation and expression of the ecdysteroid-inducible angiotensin-
RT converting enzyme-related gene in wing discs of Bombyx mori.*;
RL Insect Biochem. Mol. Biol. 31:97-103(2001).
DR EMBL; AB026110; BAA97657.1; -.
DR MEROFS; M02.002; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_WTPeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 648 AA; 74917 MW; 9A740AA9FCACEBF0 CRC64;

Query Match 25.4%; Score 1089.5; DB 5; Length 648;
Best Local Similarity 35.6%; Pred. No. 2.9e-71;
Matches 232; Conservative 125; Mismatches 259; Indels 35; Gaps 11;

QY 11 LVAVTAASQTIEQAK--TFLDKNHAEADLFY-----QSSLASWNYNTNITEEN 58
Db 10 LIAAVVAVFVATQGRDPDLEAREHEAREYMLHLDKATGLRKNRASTLAWEVYTSNITKEN 69
QY 59 VQNMNAGKWSAFLAEQSTLAQMYPLQETONLTVKLQALQNGSSVLSEDKSKRLMT 118
Db 70 EKSTQTHLELSQEAARAEETKMYGMQDFODFTLRMRFKYSQSLGVAAALPDDKQFALMR 129
QY 119 ILNTWSTYSTGKVCVNDPNOEC--LLEPGLEINELMANSLDYNERLWAESEVCKQLR 177
Db 130 TVSGHESNATACIKCYKNEKSCDLSLEPEITELFTSTSQDPEELKHAWEVHNAAGATAK 189

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QY 178 PLYEEYVVLKNEAMRANHEDYGDYWRGDEVNGVDGYDYSRGLQIEDVEHTEEIKPLY 237
Db 190 KNFTDYNLYNEAAKLNFGFNDVAEMWQSEVEVPDFE-----EQAKLWEDVKPLY 239
QY 238 EHLHAYVRKALMAY--PSYISPIGCLPAHLGLCDWGRFWTNLYSLTVFPGQKPNIDVTOA 296
Db 240 QQLHAYVRKRLDKYGDKVVSARGPIPAHLGLGNMAQTWNWNIESTRYPYDPKKEIDVTOA 299
QY 297 MYDQAWDAQRIKFAEAEKFFVSVGLPNNMTQGFWNSMLTDPCNVOKAVCHPTADWLGGK--D 355
Db 300 MRDQNTPKMFQMSDEFFRSLNLTAMPKFWKSIIEKPTD--REIVCHASAWDFFDGED 358
QY 356 FRILMCTKVTMDDFLTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVEGMSLSAATP 415
Db 359 PRIKQCTTVDYEFQTHHEMGIQYLYQYRDQPVVRDGANQGFHEAVGDTIALSVSSP 418
QY 416 KHLKSTGLSPDFQEDNTEINFLKQALTVIGTLPFTYMLEKRWVWFKGEIPKQDMKK 475
Db 419 KHLRRVGLATGD--AEDEQTEINQLYKMGIDKIAFLPEAYTLDLFRYGVFRKRLTPEDYNC 477
QY 476 KWEMKREIVGVVPPVPHIDETCYCDPASLFHVSNDYSFIRYTRTYLQFOEQEALCO--AAK 534
Db 478 HYWKLRQQLQGVPEPPVNRTEDEDDFAAAKYHVSSKVEYARYVYVSIIOFQFHRGVQQLAGE 537
QY 535 HEG----PLHKCDISNSTEAGOKLFNMLRLGKSEPTWFLALENVVGAKNMVRPLLNLYFE 589
Db 538 HAAGDPNKKLVDCDIYQSVAAAGNALANMLKMGSSKPPWDAMEALTQGRMKADGLLEYFR 597
QY 590 PLFTWLKQDNKNS--FVGMSTWSPYADQSIKIRISLKSALGDKAYEWNDN 638
Db 598 PLHDMURAENQRTGEHIGWEPTNWEYCTPQSLSELNVKEPSSSPATQOSDS 648

RESULT 11
Q9NKE4 ID Q9NKE4 PRELIMINARY; PRT; 615 AA.
AC Q9NKE4; OSVJY3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANCE PROTEIN (LD11258P).
GN ANCE OR BG:DS08220.3 OR CG8827.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT *An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.*;
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomoton M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.U., Rubin G.M.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

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Db 36 LATLSNVSAIKDEAMGVAFIEGLNDPPTTINNVDSSSWDYASNTIDYN-QNMSNKVST 94
QY 68 KWSAFLKEQSTLAQMPYLOETONLVKLOLQALQONGSSVLSBDSKRLTILNTMTSTIY 127
Db 95 EVSKMERQFGTARFEDHNFKNDSKLKLFHVAITGLAALPDDKLENATSLSKMAAY 154
QY 128 STGKVC---NPDNPQECULLPGLNEIMANSLDYNERLWAWESWRSEVQKOLRPLYEYV 184
Db 155 GSTKVTYGVKKDLP-----LEPDLTRNMKEVGNIDKLQTLAWHNAVGAIRKQYIPIY 209
QY 185 VLKNEMARAHYEDYDGYWRGDIYGVNGVDYDYSRQGLIEDYEHTEETKPLVEHLHAYV 244
Db 210 KLSNEAASLDGYDNKSAWLSDYETE-----NMTEIVDKLWEDISPLYKKLHAYV 259
QY 245 RAKLMNAYPSYISPIGCLPAHLGLDMGCRFWNTLY-SLTVPFQKPNIDVTDAMVDQAWD 303
Db 260 RMKLREIYPCRLPEDGTIPAHLLGNMWAQEWCTLYPHLTME--DKP-LDISKTMVEQKWD 316
QY 304 AORIFKEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362
Db 317 AQKMFHAEDFTSLGLDNMTSEFMSKSILT'KPED-REIQCHASAWMYNGDDFRIMKCT 375
QY 363 KVTMDPDLTAHHEMGIHQYDMAYAAQPFLLRNGANEGHEAVEGEINSLSAATPKHLKSIG 422
Db 376 DPSVEELRTVHHEMGIHYEYQYKHLHVLOEGANEGRHEAVGDDLALSATKTHYGLS 435
QY 423 LLSPDFQEDNETEINFLKQALITVGLTPTFTYMLEKRWMMVFKEIPKDWKKWEMKR 482
Db 436 LLKP---TDKYNVDDLMSALDKIAFLPFGYLLDKRWITITGETPFDMKEKFWYRI 492
QY 483 EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYRTLYQFQFQALCOAAK---HEGPL 539
Db 493 KYOGVSPVVRKNESEFFDGGAKYHVALHVPYLYRFVAFILQFQFHEHLCITVAKKVDHHPF 552
QY 540 HKCDISNSTAGQKLFNMLRLGKSEPTLALENVVGAKNMNVRLNYPEPLFTWLKQDN 599
Db 553 HECDIYGEKNAGDVLKGLSLGRSKPWPVLEIMAGTROMSASSLKKYKYEPLKWLDERI 612
QY 600 KNSFVGW 606
Db 613 KNEVGW 619

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RESULT 13
Q24222 PRELIMINARY; PRT; 630 AA.
AC Q24222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE METALLOPEPTIDASE (ANGIOTENSIN-CONVERTING ENZYME-RELATED PROTEIN).
GN ACER OR CG10593.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97128790; PubMed=8973330;
RA Taylor C.A.M., Coates D., Shirras A.D.;
RT *The Acer gene of Drosophila codes for an angiotensin-converting
RT enzyme homologue.*;
RL Gene 181:191-197(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Celniker S.E., George R.A., Galle R., Svirkas R.R., Hoskins R.A.,
RA Agbayani A., Arcana T.T., Baxter E., Blazef R.G., Chavez C., Chew M.,
RA Doyle C.M., Farfan D.E., Flanagan J., Houston K.A., Hummasti S.R.,
RA Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A., Mak J.,
RA Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M.,

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RA Park S., Pfeiffer B., Punch E., Snir E., Twomey B., Wan K.H.,
RA Whitelaw K.R., Yee A., Zhang R., Zieran L.D., Kimmel B.E.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96913; CAA65632.1; -.
DR EMBL; AC004728; -. NOT ANNOTATED_CDS.
DR FlyBase; FBgn016122; Acer.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR PRODOM; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT CONFLICT 236 L -> F (IN REF. 2).
FT CONFLICT 341 Q -> H (IN REF. 2).
FT CONFLICT 528 V -> A (IN REF. 2).
SQ SEQUENCE 630 AA; 73042 MW; 248A4B90319BC32D CRC64;

Query Match 24.0%; Score 1030; DB 5; Length 630;
Best Local Similarity 35.6%; Pred. No. 6,3e-67;
Matches 219; Conservative 113; Mismatches 260; Indels 24; Gaps 10;

QY 6 WLLLSLVAVTAAGSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQNMNA 65
Db 16 WLPGLSLMSGNSCSAVLE-ARRFELENEQLRRRFEFLSGYNYNTNVTANRQAMIEV 74
QY 66 GDKWSAFLKEQSTLAQMPYLOETONLVKLOLQALQONGSSVLSBDSKRLTILNTMTST 125
Db 75 YARNAELNKLAAQIKSSDYVQSEDADIRQAHLKLGASALNADDYLAQNALISSMOT 134
QY 126 IYSTGKVCNPDNPOEC-LLEPGLNEIMANSLDYNERLWAWESWRSEVQKOLRPLYEYV 184
Db 135 NYATATVCSYTRNSDCSLTLEPHIQERLSHSDRPAELAWYREWHDKSGTPMRQNAEYV 194
QY 185 VLKNEMARAHYEDYDGYWRGDIYGVNGVDYDYSRQGLIEDYEHTEETKPLVEHLHAYV 244
Db 195 RLTRKASQLNGHRSYADYVWQFYE-----DPDFER-----QLDATFKQLLPLYRLHGV 244
QY 245 RAKLMNAY-PSVISPTIGCLPAHLGLDMGCRFWNTLYSLTVPFQKPNIDVTDAMVDQAWD 303
Db 245 RFLRQHYGPDVMPAEGNIPISLGNMWSQSNELLDTPTYPEKPFYDVYKAEKQGYT 304
QY 304 AORIFKEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362
Db 305 VQKLELGDQFFQSLGMRALPPSPFNLSVLT'RPDD-RQVYCHASANDFYQSDVRIKMT 363
QY 363 KVTMDPDLTAHHEMGIHQYDMAYAAQPFLLRNGANEGHEAVEGEINSLSAATPKHLKSIG 422
Db 364 EVDSHYFYVHHHELGHIIQYLYQYEQQPAVYRGAPNPGPFHEAVGDIYALSVAKHLKIG 423
QY 423 LLSPDFQEDNETEINFLKQALITVGLTPTFTYMLEKRWMMVFKEIPKDWKKWEMKR 482
Db 424 LIE-NGLRDEKSRINQLFKOALSKIVLFPFGYAVDKYRYAVFRNELDESQNGCFQWMS 482
QY 483 EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYRTLYQFQFQALCOAAKHEGP---- 538
Db 483 EFGGVPEVPFRTEKDFDPKAKHIDADVLEIRYFAAHIFQFQFKVLCRKAGQYAPNNSR 542
QY 539 --LHKCDISNSTAGQKLFNMLRLGKSEPTLALENVVGAKNMNVRLNYPEPLFTWLK 596
Db 543 LTLNDCDIFGSKAAGSLSQFLSKGNSRHWKEVEETGETEMDPAALLEYFEPLYQWLK 602
QY 597 DQNKNSFFGWSTWSP 612
Db 603 QE--NSRLGVLGWGP 616

RESULT 14
Q9VLJ6 PRELIMINARY; PRT; 630 AA.
AC Q9VLJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE ACER PROTEIN (LD28328P).  
GN ACER OR CG10593.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer J.D., Zhang Q., Chen L.X.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT The genome sequence of *Drosophila melanogaster*.;  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Y, CN BW SP;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE03621; AAF52693.1;  
DR EMBL; AY051750; AAK93174.1;  
DR MEROPS; M02.002;  
DR FlyBase; FBgn0016122; Aعر.  
DR InterPro; IPR001548; Peptidase\_M2.  
DR InterPro; IPR000130; Zn\_Mpeptidse.  
DR Pfam; PF01401; Peptidase\_M2; 1.  
DR PRINTS; PR00791; PEPTIDASEA.  
DR ProDom; PD004184; Peptidase\_M2; 1.  
DR PROSITE; PS00142; 2INC\_PROTEASE; UNKNOWN.1.  
SQ SEQUENCE 630 AA; 73057 MW; 6D93355EB57773289 CRC64;  
Query Match 24.0%; Score 1028; DB 5; Length 630;  
Best Local Similarity 35.6%; Pred. No. 8.9e-67;  
Matches 219; Conservative 112; Mismatches 261; Indels 24; Gaps 10;

QY 6 WLLSLVAVTAQAQTEIOAKTFLDKFNHEAEDLFYOSSLASWNYNTNITENYQNKNA 65  
Db 16 WLPGLSGMNGSCSASVLE-ARRFFELENEQLRRRFFHEFLSGYNYNTNITENYQNAMLEV 74  
QY 66 GDKWSAFLKEQSTLAQMPYLOBIQNLTVKLQALQALQONGSSVLSSEKSKRLNTILNTMST 125  
Db 75 YARNAELNKRLAQKISSDYVQSEDADIRQAEBHLSKLGASALNADDYALQNAISSMOT 134  
QY 126 IYSTGKVCNPNQEC-LLEPGLNIMANSLDYNERLHAWESWRSEVGKOLRPLYEYV 184  
Db 135 NVATATVCSYTNRSDCSLTLEPHIOERLSHRDPAELAWYREWHDKSGTMRONFAEYV 194  
QY 185 VLKNEMARANHYEDGYWRGDEYVNGVDYDSRGGLIEDVEHTFEIKPLYEHLHAYV 244  
Db 195 RLTKASQNGHRSYADYVWQYFE-----DPPFER-----QLDATTFKQLLPFYQLHGYV 244  
QY 245 RAKLMNAY-PSYISPTGCLPAHLIGDMWGRFNLXSLTVPFGQKPNIDVTDAMVDQAWD 303  
Db 245 RFLRQHYGPDYMPAEGNIPISLGNMGOSWNELLDLFTYPEKPFVDVKAEMEKGCT 304  
QY 304 AQRIKFAEKFFVSVGLPNMTGFWNSMLTDPGNVOKAVCHPTAWDLGK-GDFRILMCT 362  
Db 305 VOKLPELGDQFFQSLGMRALPPSFNLSVLTTPDD-RHVYCHASAWDFYQSDVRIKMT 363  
QY 363 KVTMDLTAHEMGGHIQYDMAYAAOPFLRNGANGEGFHEAVGEIMSLSAATPKHLKSG 422  
Db 364 EVDSHYFYVHHELGHIIQYLYQEQQPAVYRGAPNPGFHEAVGDIUALSVWSAKHLKALG 423  
QY 423 LLSLPQFQEDNEINFLKQALITVGLPTPTMLEKRWVFKGEIPKDDONKMKWEMKR 482  
Db 424 LIE-NGLRDEKSRINQLFKQALSKIVFLPGYAVDKYRYAVFRNELDSESONNCGFWQRS 482  
QY 483 EIVGVVEVPHPDTCYPASLHFVSNDSYIRYTRTYLQFQFQALCAAKHEGP----- 538  
Db 483 EGGVEPPVTEKEDPPAKYHIDADVEYLRYFAAHIFQFQFKALCKRGAQYAPNNSR 542  
QY 539 --LHKDCISNSVENGOKLFNMLRKGSEPTWLALENVGAKNMVRLINLYFELFTWLK 596  
Db 543 LFLDNCIDFGSKAAGSLSQFLSKGSRHWKEVLEETGETEMDPAALLEYFEPYQWLK 602  
QY 597 DQNKNSFCVGSWTDSWP 612  
Db 603 QE-NSRLGVPCWGP 616  
RESULT 15  
Q9D836 PRELIMINARY; PRT; 249 AA.  
AC Q9D836  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 2010305L05RIK PROTEIN.  
GN 2010305L05RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
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RL Nature 409:685-690(2001).
DR EMBL; AK008530; BAB25723.1; -.
DR MGD; MGI:1917258; 2010305L05Rik.
DR InterPro; IPR001548; Peptidase_M2.
DR ProDom; PD004184; Peptidase_M2; 1.
SQ SEQUENCE 249 AA; 28379 MW; 19372B2B78AAE921 CRC64;

Query Match 23.4%; Score 1004; DB 11; Length 249;
Best Local Similarity 75.1%; Pred. NO. 1.3e-65;
Matches 187; Conservative 31; Mismatches 31; Indels 0; Gaps 0;

QY 557 MLRLGKSEPTWLTALENVVCAKMMNVRLPLNYPEPLFTWLKQNKNSFVGWSTDSVPYADQ 616
Db 1 MLSLGSEPTWLTALENVVCAKMMNVRLPLNYPEPLFTWLKQNKNSFVGWSTDSVPYADQ 60

QY 617 SIKVRISLKSALGDKAYEWNDEMFLRSVAYAMQYFLKVKKNQMLFGCEDVRVANLK 676
Db 61 SIKVRISLKSALGANAYEWNDEMFLRSVAYAMQYFLKVKKNQMLFGCEDVRVANLK 120

QY 677 PRISFNFTAPKNVSDIIPRTEVEKAIKMSRSRINDAPRLNDNSLEFLGCTQTLGPPNQ 736
Db 121 PRVSFFFTSPQNVSDVIPRSEVEDAIRMSRGRINDVFLGNDNSLEFLGIHPTLEPPYQ 180

QY 737 PPVSTWLIVGVGMGVIVVIGVILIFTGIRDRKKKARKSGENPYASIDISKGENNPFQ 796
Db 181 PPVTIWLIIFGVVMALVVVGIIILIVTGIRKKKARKETKRENSYDSMDIGKGESNAGFQ 240

QY 797 NTDDVQTSF 805
Db 241 NSDDAQTSF 249
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Search completed: October 9, 2002, 17:55:06  
Job time : 74 secs

